AMENDMENT

It is respectfully requested that the application be amended without prejudice, without admission, without surrender of subject matter, and without any intention of creating any estoppel as to equivalents, as follows. Attached hereto is a marked up version of the changes made to the specification by this amendment. The attachment is captioned "**Version With Markings to Show Changes Made.**"

IN THE SPECIFICATION

Please amend the specification without prejudice, without admission, without surrender of subject matter, and without any intention of creating any estoppel as to equivalents as follows:

Please replace the paragraph beginning on page 60, line 7 with the following rewritten paragraph:

-- The DNA sequence of the regions flanking the integrated copy of TCa2 was also determined (not shown). Starting about 800 bp upstream of the retrotransposon is sequence virtually identical to that of the 5' regions of the *C. albicans* CDR1 gene (Prasad et al 1995), which has been assigned to chromosome 3. About 100 bp downstream is the start of an ORF that bears a strong resemblance to the 5' regions of cytoplasmic dynein heavy chain genes found in some other fungi. A *C. albicans* sequence containing an ORF that bears a strong resemblance to the central region of other fungal cytoplasmic dynein heavy chain genes has previously been assigned to chromosome 3. These findings indicate that the cloned copy of TCa2 is located on chromosome 3, between CDR1 and a gene encoding cytoplasmic dynein heavy chain. Using PCR and primers corresponding to sequences on either side of the TCa2 integration site we were able to amplify and sequence, from hOG759, another allele without an integrated retrotransposon. This work revealed, therefore, that this locus is heterozygous for the presence of TCa2, and it also showed that the insertion of TCa2 resulted in a duplication of 5 bp (ACACG) at the integration site, as is commonly found with other retrotransposons. --

Please replace the paragraph beginning on page 80, line 26 with the following rewritten paragraph:

-- In order to 'tag' the retrotransposon the intention was to use an inverted ('back to front') intron inserted within a reporter gene (URA3). Such an inverted intron would prevent URA3 phenotypic function unless the intron is removed from the transcript (Figure 73). --